


```

; CURRENT APPLICATION NUMBER: US/09/880-708
; BEST LOCAL STABILITY: 99.24; Pred. No. 6.4e-62;
; PRIOR APPLICATION NUMBER: P02/09/06/03065
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: DR/195 25 416.3
; NUMBER OF SEQ. ID NOS: 7
; SOFTWARE: PctIn version 3.1
; SEQ ID NO: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-708-1

Query Match 99.4%; Score 640; DB 8; Length 501;
Best Local Stability 99.24; Pred. No. 6.4e-62;
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLATGCGPCKKAKRCAKRALVNFQMGNDWIAPIETAFHCEIGCEPFLSHLE 60
Db 333 PLATGCGPCKKAKRCAKRALVNFQMGNDWIAPIETAFHCEIGCEPFLSHLE 60
383 PLATGCGPCKKAKRCAKRALVNFQMGNDWIAPIETAFHCEIGCEPFLSHLE 442
Qy 61 PTHNAVITLANSNDPSTPPCVPTFFHSTILIFTSANNNVYKQIEMVYEQCR 119
Db 443 PTHNAVITLANSNDPSTPPCVPTFFHSTILIFTSANNNVYKQIEMVYEQCR 501

RESULT 5
US-09-880-708-13
; Sequence 13, Application US/09880708
; Patent No. 082000155361AI
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQ. ID NOS: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Gary Ware & Freldegarich LLP
; STREET: 435 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; CONVERTING IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880-708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: 12-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 38,347
; FILING DATE: 12-JUN-1993
; INFORMATION FOR SEQ ID NO: 13:
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELEPHONE: 619/677-1465
; TELEFAX: 619/677-1466
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; IMMEDIATE SOURCE:
; CLONE: GDN-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-880-708-13

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Query Match 98.4%; Score 640; DB 10; Length 119;
Best Local Stability 98.34; Pred. No. 4e-61;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLATGCGPCKKAKRCAKRALVNFQMGNDWIAPIETAFHCEIGCEPFLSHLE 60
Db 337 PLATGCGPCKKAKRCAKRALVNFQMGNDWIAPIETAFHCEIGCEPFLSHLE 436
61 PTHNAVITLANSNDPSTPPCVPTFFHSTILIFTSANNNVYKQIEMVYEQCR 119
Db 437 PTHNAVITLANSNDPSTPPCVPTFFHSTILIFTSANNNVYKQIEMVYEQCR 495

RESULT 6
US-09-880-708-10
; Sequence 10, Application US/09880708
; Patent No. 082000155361AI
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQ. ID NOS: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Gary Ware & Freldegarich LLP
; STREET: 435 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121-2189
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; CONVERTING IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,708
; FILING DATE: 12-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/145,060
; FILING DATE: <known>
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 38,347
; FILING DATE: 12-JUN-1993
; INFORMATION FOR SEQ ID NO: 10:
; REFERENCE/DOCKET NUMBER: 07265/057002
; TELEPHONE: 619/677-1465
; TELEFAX: 619/677-1466
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; IMMEDIATE SOURCE:
; CLONE: GDN-5
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-880-708-10

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[illegible]

[illegible]

[illegible][illegible]

Search completed: September 26, 2003, 17:57:14
Job time : 24 secs

[illegible]

[illegible]

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148	NHIVTAVSYVNDVAILKFAKCVPELASHLSTLEISANNVYVYKOTEDVYVSCOR 204	
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genome version 5.1.6
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ON protein - protein search, using sw model

Run on: September 26, 2003, 17:42:43 : Search time 84 Seconds

(without alignments)
224.867 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATGQKRSKMLKACSR.....ANNVYQKEDWVMSGCR 119

Scoring table: ELSDN62

Gapop 10.0 : Gapext 0.5

Searched: 1107863 seqs, 15872573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_320m30*

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- 2: /SIDSL/sgcdgta/geneseq/emb1/AA1981.DAT.*
- 3: /SIDSL/sgcdgta/geneseq/emb1/AA1982.DAT.*
- 4: /SIDSL/sgcdgta/geneseq/emb1/AA1983.DAT.*
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- 7: /SIDSL/sgcdgta/geneseq/emb1/AA1986.DAT.*
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- 22: /SIDSL/sgcdgta/geneseq/emb1/AA2001.DAT.*
- 23: /SIDSL/sgcdgta/geneseq/emb1/AA2002.DAT.*
- 24: /SIDSL/sgcdgta/geneseq/emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	645	99.4	119	119	AA1980	Human MF52	
2	645	99.4	119	119	AA1981	Human MF52	
3	645	99.4	119	119	AA1982	Human bone	
4	645	99.4	120	120	AA1983	Human bone	
5	645	99.4	120	120	AA1984	Human bone	
6	645	99.4	120	120	AA1985	Human bone	
7	645	99.4	120	120	AA1986	Human bone	
8	645	99.4	120	120	AA1987	Human bone	
9	645	99.4	120	120	AA1988	Human bone	

10	645	99.4	501	18	AA1989	Human MF52	
11	645	99.4	501	18	AA1990	Human TGF-beta p10	
12	645	99.4	501	18	AA1991	Human TGF-beta p10	
13	645	99.4	501	18	AA1992	Human TGF-beta p10	
14	645	99.4	501	18	AA1993	Human TGF-beta p10	
15	645	99.4	501	18	AA1994	Human TGF-beta p10	
16	645	99.4	501	18	AA1995	Human TGF-beta p10	
17	645	99.4	501	22	AA1996	Human TGF-beta p10	
18	645	99.4	501	22	AA1997	Human TGF-beta p10	
19	645	99.4	501	22	AA1998	Human TGF-beta p10	
20	645	99.4	501	22	AA1999	Human TGF-beta p10	
21	645	99.4	501	22	AA2000	Human TGF-beta p10	
22	645	99.4	501	22	AA2001	Human TGF-beta p10	
23	645	99.4	501	22	AA2002	Human TGF-beta p10	
24	645	99.4	501	22	AA2003	Human TGF-beta p10	
25	645	99.4	501	22	AA2004	Human TGF-beta p10	
26	645	99.4	501	22	AA2005	Human TGF-beta p10	
27	645	99.4	501	22	AA2006	Human TGF-beta p10	
28	645	99.4	501	22	AA2007	Human TGF-beta p10	
29	645	99.4	501	22	AA2008	Human TGF-beta p10	
30	645	99.4	501	22	AA2009	Human TGF-beta p10	
31	645	99.4	501	22	AA2010	Human TGF-beta p10	
32	645	99.4	501	22	AA2011	Human TGF-beta p10	
33	645	99.4	501	22	AA2012	Human TGF-beta p10	
34	645	99.4	501	22	AA2013	Human TGF-beta p10	
35	645	99.4	501	22	AA2014	Human TGF-beta p10	
36	645	99.4	501	22	AA2015	Human TGF-beta p10	
37	645	99.4	501	22	AA2016	Human TGF-beta p10	
38	645	99.4	501	22	AA2017	Human TGF-beta p10	
39	645	99.4	501	22	AA2018	Human TGF-beta p10	
40	645	99.4	501	22	AA2019	Human TGF-beta p10	
41	645	99.4	501	22	AA2020	Human TGF-beta p10	
42	645	99.4	501	22	AA2021	Human TGF-beta p10	
43	645	99.4	501	22	AA2022	Human TGF-beta p10	
44	645	99.4	501	22	AA2023	Human TGF-beta p10	
45	645	99.4	501	22	AA2024	Human TGF-beta p10	

ALIGNMENTS

RESULT 1
AA14236
AA14236
AA14236 standard; Protein; 119 AA.

AC AA14236;
29-FEB-2000 (first entry)

DE Mutant human MF52 monomer protein.

DE Mutant MF52 monomer protein; transforming growth factor-beta; TGF-beta;

DE PCOT272 expression vector; osteocyte; bone morphogenetic; osteopapillo;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

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DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

DE osteoblast; osteocyte; osteocyte; osteocyte; osteocyte; osteocyte;

Key Location/Qualifiers

FF Match

FF Match

FF Match

FF Match

FF Match

FF Match

FF Match

FF Match

FF Match

XX Kawai S, Kimura M, Muraki Y, Katsura M:
 XX WPI; 2000-097122/08.
 XX N-PSDB; AA299328.
 XX Novel monomer protein used for prevention and treatment of bone and/or
 XX cartilage diseases.
 XX
 XX Claim 4; Page 20; 26pp; English.
 XX
 XX The present sequence is a mutant human MP52 monomer protein, which
 XX belongs to transforming growth factor-beta (TGF-beta) family by
 XX transforming them with pGCR279 expression vector containing a mutated
 XX MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is
 XX a member of transforming growth factor-beta (TGF-beta) family, and has
 XX morphogenetic, osteogenic and anti-arthritis activity. The MP52 monomer
 XX protein is used for prevention and treatment of cartilage and/or bone
 XX diseases such as osteoporosis, osteoarthritis, rheumatoid arthritis, damage of
 XX articular cartilage, fracture, congenital bone and/or cartilage diseases
 XX and tumor dissection, fracture, congenital bone and/or cartilage diseases
 XX such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis
 XX and hypoplasia and a deficit of root of teeth and a tooth socket.
 XX Sequence 119 AA:
 XX
 XX Query Match 100.0%; Score 649; DB 21; Length 119;
 XX Best Local Similarity 100.0%; Pred. No. 6.9e-50;
 XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PLATGQSEKSNKAKSKALFNKDMGDMQWIMATFYKRCRCEFLPSHLE 60
 DB 1 PLATGQSEKSNKAKSKALFNKDMGDMQWIMATFYKRCRCEFLPSHLE 60
 QY 61 PTHNAVITLANSNDSPFPACVPTPLSPFLTSDANVYKTYKTYWVSSGCR 119
 DB 61 PTHNAVITLANSNDSPFPACVPTPLSPFLTSDANVYKTYKTYWVSSGCR 119
 XX
 XX RESULT 2
 XX ID AAM06920 standard; Protein: 119 AA.
 XX AAM06920:
 XX 27-JUN-1997 (first entry)
 XX Human MP52 growth factor residues 383-501.
 XX Human; MP52; growth factor; monomer; dimer; treatment; bone;
 XX cartilage; dental; disorder; fracture; bone loss;
 XX periodontal disease; calcification; osteoporosis.
 XX OS Homo sapiens.
 XX W0953215-AL.
 XX 24-OCT-1996.
 XX 19-MAR-1996; 96NO-JP01062.
 XX WPI; 1996-445730/46.
 XX N-PSDB; AA46150.
 XX
 XX Katsura M, Kawai S, Kimura M, Muraki Y, Takamatsu H:
 XX WPI; 1996-445730/46.
 XX N-PSDB; AA46150.

XX Peptide consisting of part of human MP52 growth factor, and its
 XX dimer, is used for treatment of bone, cartilage and dental
 XX disorders.
 XX
 XX Claim 1; Pages 18-19; 33pp; Japanese.
 XX
 XX The present sequence is residues 383 to 501 of the human MP52
 XX growth factor, a dimer of which can be used to treat bone,
 XX cartilage and dental disorders, including fractures, bone loss and
 XX periodontal disease, calcification, osteoporosis, and including most
 XX (preferably all) cells with a suitable plasmidly expression vector
 XX containing DNA encoding the monomer. The host was cultured, and
 XX inclusion bodies from the cells worked up to give the monomer, with
 XX type 1 919 tendon collagen and injected into the large thigh vein
 XX of the rat. After 20 days 4 of 4 mice injected with 10 microl of
 XX the dimer showed bone/cartilage calcification around the injection
 XX sites, compared to none in 0 of 4 mice treated with collagen only.
 XX Sequence 119 AA:
 XX
 XX Query Match 99.44; Score 645; DB 17; Length 119;
 XX Best Local Similarity 99.74; Pred. No. 1.0e-59;
 XX Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATGQSEKSNKAKSKALFNKDMGDMQWIMATFYKRCRCEFLPSHLE 60
 DB 1 PLATGQSEKSNKAKSKALFNKDMGDMQWIMATFYKRCRCEFLPSHLE 60
 QY 61 PTHNAVITLANSNDSPFPACVPTPLSPFLTSDANVYKTYKTYWVSSGCR 119
 DB 61 PTHNAVITLANSNDSPFPACVPTPLSPFLTSDANVYKTYKTYWVSSGCR 119
 XX
 XX RESULT 3
 XX ID AAM19846 standard; Protein: 119 AA.
 XX AAM19846:
 XX 12-FEB-1998 (first entry)
 XX Human bone inducing factor MP52.
 XX Human; bone inducing factor; MP52; collagen; fracture;
 XX polyoxyethylene-polyoxypropylene glycol.
 XX OS Homo sapiens.
 XX W0718829-AL.
 XX 29-MAY-1997.
 XX 14-NOV-1996; 96NO-JP03133.
 XX 17-NOV-1995; 95JP-0322402.
 XX (PARK) ROCHIST JAPAN LTD.
 XX (PARK) ROCHIST PHARM & CHEM KK.
 XX Shimura T, Toriyama S;
 XX WPI; 1997-310243/28.
 XX N-PSDB; AAM70296.
 XX
 XX Material for repairing bone and collagen, especially bone fracture
 XX or loss - comprising bone-inducing factor and
 XX polyoxyethylene-polyoxypropylene glycol compounds
 XX Example 4; Page 16-17; 31pp; Japanese.
 XX Bone and collagen inducing material has been developed which comprises
 XX bone inducing factor and polyoxyethylene-polyoxypropylene glycol

CC compounds. The Present sequence represents human bone inducing factor
 CC MP52. This material allows treatment without surgery. It is highly
 CC and undergoes reversible sol-gel transition depending on the
 CC temperature.
 CC Sequence 119 Aa;

Query Match 99.4%; Score 645; Db 16; Length 120;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 60
 DB 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 60
 QY 61 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 119
 DB 61 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 119

RESULT 4

AAAF8731
 ID AA026550 standard; Protein; 120 Aa.

XX AA026550;
 AC AA026550;
 DT 25-MAR-2003 (updated)
 DT 23-MAY-1995 (first entry)

XX Murine protein MP52.
 DE

XX Bone morphogenetic protein; MP52, tendon; ligament.
 KW
 XX Mus musculus.
 XX
 XX 15-JUN-1995.
 XX 06-DEC-1994; 94NO-U514030.
 XX 02-MAY-1984; 94US-033576.
 XX 07-DEC-1993; 93US-014103.
 XX 25-MAR-1994; 94US-0217780.
 XX (GENE) GENETICS INST INC.
 XX (HARD) HARVARD COLLEGE.

XX Coleste AZ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 P1 Kennedy JM.
 XX MP1: 1995-224320/29.
 XX N-PM50; AA0696209.

XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 XX example. For inducing tendon/ligament-like tissue formation
 XX P5
 XX Page 51-52; 84pp; English.

XX Oligos #6 and #7 (AA0696218 & AA0696219) are used as primers for the
 XX amplification of a 275 bp DNA probe. The internal 269 bp of which
 XX corresp. to nt #607 to #863 of AA0696207, from the BMP-12 encoding
 XX cDNA plasmid subclone PCN-12. This probe was radioactively labelled
 XX with ³²P and used for Southern blot hybridization. The results
 XX of one of positively hybridising recombinants named MP52 indicates
 XX that it encodes a portion of the mouse gene corresp. to the PCR
 XX product MPV (murine homolog of the MP-52 sequence AA0696209/973731).
 XX (Updated on 25-MAR-2003 to correct PM field.)

XX Sequence 120 Aa;

Query Match 99.4%; Score 645; Db 16; Length 120;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 60
 DB 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 60
 QY 61 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 119
 DB 61 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 120

RESULT 5

AAAF8731
 ID AA026550 standard; Protein; 120 Aa.

XX AA026550;
 AC AA026550;
 DT 25-MAR-2003 (updated)
 DT 21-JAN-1998 (first entry)

XX Human MP52 protein.
 DE

XX MP52, BMP7, bone morphogenetic protein; human; tendon; ligament;
 KW bone inducing; tissue repair; tendonitis; carpal tunnel syndrome;
 XX therapy.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX PT Protein 1..120
 XX PT Protein 19..120 Claim 5*
 XX FT Protein /note= "Claim 5*"
 XX US555882-A.

XX 19-AUG-1997.
 XX 22-DEC-1994; 94US-0362670.
 XX 22-DEC-1994; 94US-0362670.
 XX 25-MAR-1994; 94US-0217780.
 XX 25-MAR-1994; 94US-0217780.
 XX 02-NOV-1994; 94US-033576.
 XX (GENE) GENETICS INST INC.
 XX (HARD) HARVARD COLLEGE.

XX Coleste AZ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 P1 Kennedy JM.
 XX MP1: 1997-124270/39.
 XX Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
 XX - useful for tissue healing and repair; treatment of tendonitis,
 XX improving fixation of tendons to bone etc
 XX Claim 5; Column 39-40; 43pp; English.

XX This polypeptide comprises human MP52. A claimed method for
 XX inducing formation of tendon and/or ligament tissues involves the
 XX administration of a composition containing at least one protein
 XX selected from MP52, BMP-12 (see AA026559) and BMP-13 (see AA026551).
 XX This method is useful for the treatment of tendon and ligament
 XX tissues. This method is also useful for the treatment of tendonitis
 XX and other defects of traumatic or congenital origin, in cosmetic
 XX surgery and to improve fixation of tendons or ligaments to bone.
 XX MP52, e.g., BMP-7 (see AA026559) can be used to increase activity of other
 XX (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 120 Aa;

Best Local Similarity 99.2%; Fred. No. 1.8e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 60
 DB 1 PAAATGKFSKSLAKSKALAVKNGMDWIAFLFAFATGSCGCPFLSHLE 61
 QY 61 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 119
 DB 62 PPNNAVITLMSNGDPTFCVPTPLSP ILIFSDANNVYKQEMVYVSCQR 120

CC tissue, skin, mucosa, epithelium or dental tissue. The protein can also
 CC be used for wound healing and tissue regeneration e.g. in osteoporosis
 CC (based on 25-MAR-2003 to correct FN field.)

XX
 50 Sequence 501 AA: 99.4%; Score 645; DB 18; Length 501;
 Query Match
 Best Local Similarity 99.2%; Pred. No. 1e-58; 1; Indels 0; Gaps 0;
 Matches 118; Conservative 0; Mismatches 0;

QY 1 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 60

DB 383 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 442

QY 61 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 119

DB 443 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 501

RESULT 10

ID AMN36100 standard; Protein; 501 AA.

XX
 AC AMN36100;

XX 08-MAR-1998 (first entry)

XX Human MP52.

XX Bone morphogenetic protein; BMP; processing enzyme; MP52;

XX BMP-2; BMP-4; BMP-6; BMP-7; Bone formation; Bone regeneration.

XX Homo sapiens.

XX W9741250-AL.

XX 06-MAR-1997.

XX 28-APR-1997.

XX 30-MAR-1996; 9637-0130618.

XX (FARH) HOECHST VAUGHN KOGYO KK.

XX (FARH) HOECHST PHARM & CHEM KK.

XX Kimura M, Makishima F, Takahashi M;

XX NPY, 1997-547168/50.

XX N-PEBP; AN796131.

XX Production of mature bone morphogenetic protein - by treatment of

XX directly or by expressing them both in the same host

XX

XX Example 1; Pages 21-25; 34pp; Japanese.

XX The present sequence is MP52, which is a bone morphogenetic

XX protein (BMP). It is produced by directly adding a BMP processing

XX enzyme to a solution containing BMP precursor protein or by

XX transforming an animal cell with expression vectors containing DNA

XX encoding the enzyme and precursor protein, culturing the

XX transfectants, and purifying the mature BMP protein. The

XX method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,

XX which can be used to treat bone formation or regeneration

XX abnormalities.

XX Sequence 501 AA:

XX Query Match

XX Best Local Similarity 99.4%; Score 645; DB 18; Length 501;

XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 60

DB 383 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 442

QY 61 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 119

DB 443 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 501

RESULT 11

ID AMN19210 standard; Protein; 501 AA.

XX
 AC AMN19210;

XX 04-MAR-1998 (first entry)

XX Human TGF-beta protein MP52.

XX Human transforming growth factor-beta, TGF-beta, MP52, superfamily;

XX cartilage; bone inducing activity; Inhibit, bone resorption.

XX Homo sapiens.

XX D81548476-AL.

XX 26-JUN-1997.

XX 22-DEC-1995; 95DB-1048476.

XX (HOP-) BIOPHARM GMS BIOTECHNOLOGISCHEN ENTWICKEL.

XX Bechtold B, Botten G, Paulista M, Poll J, Boettgen G;

XX W197-333931/31.

XX Compound containing protein from TGF-beta superfamily - has bone

XX and/or cartilage inducing activity, useful in treatment of; e.g.

XX osteoporosis, bone damage, Paget's disease and osteoarthritis

XX

XX Claim 3; Page 9; 10pp; German.

XX This sequence is the human transforming growth factor (TGF)-beta protein

XX designated MP52. MP52 can be used in a compound of formula (I):

XX A-x(1-20)-y(1-20) (I); A = protein, or fragment, of the TGF-beta

XX protein; B = 1 or more substituent groups with an affinity to the extracellular

XX matrix, cellular components of bone and/or cartilage and/or to a

XX receptor; C = 1 or more substituent groups with an affinity to a

XX group. The compound may be used to inhibit bone resorption, prevent or

XX treat bone or cartilage related disorders, including osteoporosis,

XX Paget's disease, osteosclerosis, osteoarthritis or osteoarthritis and

XX to treat bone or cartilage damage caused by rounding or overloading.

XX Sequence 501 AA:

XX Query Match

XX Best Local Similarity 99.2%; Score 645; DB 18; Length 501;

XX Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 60

DB 383 PLATROCKSPENKALGSKALHFWKNDKNDONTAPTEAFRCGLCEPFLSHLE 442

QY 61 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 119

DB 443 PTHNAVLOTANSDPSTPPACVPPFLSPISLIFSDANNVYKQEMWVSGOR 501

```

RESULT 12
ID AMK1300 standard; Protein: 501 AA.
XX
XX AMK1300;
XX
XX 28-OCT-1997 (first entry)
XX
XX Human high mol. wt. protein MP52, a growth/differentiation factor.
XX
XX growth factor; differentiation; bone induction; osteoporosis; teeth.
XX
XX tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
XX
XX wound healing; regeneration; skeletal disorder; fracture; dimer.
XX
XX OS Homo sapiens.
XX
XX MW3704.095-A1.
XX
XX 06-FEB-1997.
XX
XX 24-JUL-1996; 5680-JF02065.
XX
XX 24-JUL-1995; 953P-0218022.
XX
XX (FASE ) KOREST JAPAN LTD.
XX
XX (FASE ) KOREST PHARM & CHEM KK.
XX
XX Fujio Y, Kawai S, Kimura M, Matsumoto K, Takahashi M;
XX
XX WPI: 1997-132636/12.
XX
XX N-FCDS; AM51412.
XX
XX high molecular weight human MP52 growth or differentiation factor -
XX
XX promotes bone induction, is useful for treatment and prevention of
XX
XX bone disease
XX
XX Claim 1: Pages 13-16; 21pp; Japanese.
XX
XX AMK1300 is a high mol. wt. form of a human growth/differentiation
XX
XX factor MP52. MP52 promotes bone induction and is useful for plastic
XX
XX reconstructive surgery, cosmetic facial treatment, bone transplantation
XX
XX and tooth implantation. It is also useful for the treatment and
XX
XX prevention of bone disease.
XX
XX tissue, skin, mucous membranes, nails or teeth; for wound treatment and
XX
XX tissue regeneration; and for the treatment of skeletal disorders and
XX
XX fractures.
XX
XX Sequence 501 AA;
XX
XX Query Match 99.44; Score 645; DB 18; Length 501;
XX
XX Best Local Similarity 99.28; Pred. No. le-36; 1; Indels 0; Gaps 0;
XX
XX Matches 118; Conservative 0; Mismatches 1;
XX
XX QY 1 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 60
XX
XX DB 383 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 442
XX
XX QY 61 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 119
XX
XX DB 443 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 501
XX
XX RESULT 14
XX
XX AMK1770
XX
XX AMK1770 standard; Protein: 501 AA.
XX
XX AC AMK1770;
XX
XX 11-NOV-1997 (first entry)
XX
XX DE Human bone morphogenetic factor MP52 Arg
XX
XX XX Bone morphogenetic factor; MP52 Arg; bone; cartilage; skin;
XX
XX connective tissue; mucous membrane; epithelium; teeth;
XX
XX wound healing; vunerlery; tissue regeneration; osteoporosis;
XX
XX bone fracture; dental implant; osteoblast.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Peptide /Label- sig_peptide
XX
XX FT 380..381
XX
XX FT /Note- sequencing suggests MP52 Arg is processed
XX
XX FT 381..382
XX
XX FT /Note- alternative cleavage site at Arg381-Ala382*
XX
XX FT Mat_protein 381..501

```

```

Query Match 99.44; Score 645; DB 18; Length 501;
Best Local Similarity 99.28; Pred. No. le-36; 1; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 1;
QY 1 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 60
DB 383 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 442
QY 61 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 119
DB 443 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 501
RESULT 13
AMK01799 standard; Protein: 501 AA.
XX
XX AMK01799;
XX
XX 15-OCT-1997 (first entry)
XX
XX DE Human MP52 protein.
XX
XX Human; MP52; transforming growth factor; TGF; beta; medicament;

```

```

treatment; prevention; nervous system; disease; neuropathology;
ageing.
XX
XX OS Homo sapiens.
XX
XX DE1922415-A1.
XX
XX 16-2AN-1997.
XX
XX 12-JUL-1995; 95DB-1025416.
XX
XX 12-JUL-1995; 95DB-1025416.
XX
XX (JDB-) BIOHARM GDS BIOCHEMOLGOLSCHEM EFFUCL.
XX
XX Bechtold R, Roetten G, Paulista M, Pohl J, Unsicker K;
XX
XX WPI: 1997-078343/08.
XX
XX N-FCDS; AM759405.
XX
XX Medicaments contg. protein MP52 - useful for treating neurological
XX
XX disorders
XX
XX Claim 2: Pages 12-14; 21pp; German.
XX
XX The present sequence is the human MP52 protein, which is
XX
XX described in WO 9316099 and 9504819 as a member of the human
XX
XX transforming growth factor beta superfamily. Active MP52 can be
XX
XX used for the treatment and/or prevention of bone diseases,
XX
XX and/or to treat neuropathological conditions caused by nervous
XX
XX system ageing.
XX
XX Sequence 501 AA;
XX
XX Query Match 99.44; Score 645; DB 18; Length 501;
XX
XX Best Local Similarity 99.28; Pred. No. le-36; 1; Indels 0; Gaps 0;
XX
XX Matches 118; Conservative 0; Mismatches 1;
XX
XX QY 1 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 60
XX
XX DB 383 PLATQKQSPNKAACSKALVNFKMGNDNTATLPTAFPCGLCEPFLASLE 442
XX
XX QY 61 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 119
XX
XX DB 443 PTHNATVOTIANSQDSTPTCCVPTPLSLPILSDSNANNVYKQEDMVESGCR 501
XX
XX RESULT 14
XX
XX AMK1770
XX
XX AMK1770 standard; Protein: 501 AA.
XX
XX AC AMK1770;
XX
XX 11-NOV-1997 (first entry)
XX
XX DE Human bone morphogenetic factor MP52 Arg
XX
XX XX Bone morphogenetic factor; MP52 Arg; bone; cartilage; skin;
XX
XX connective tissue; mucous membrane; epithelium; teeth;
XX
XX wound healing; vunerlery; tissue regeneration; osteoporosis;
XX
XX bone fracture; dental implant; osteoblast.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Peptide /Label- sig_peptide
XX
XX FT 380..381
XX
XX FT /Note- sequencing suggests MP52 Arg is processed
XX
XX FT 381..382
XX
XX FT /Note- alternative cleavage site at Arg381-Ala382*
XX
XX FT Mat_protein 381..501

```


Db 2 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 61
 Qy 61 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 119
 Db 62 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 120

RESULT 2
 US-08-333-576C-4
 Sequence 4, Application US/08333576C
 Patent No. 6027519
 GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil
 APPLICANT: Thomas, Gerald R.
 APPLICANT: Neil, Douglas
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,576C
 FILING DATE: September 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-B
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617 876-5850
 TELEPHONE: 617 876-5851
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-333-576C-4
 Query Match 99.4%; Score 645; DB 3; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1,4e-64;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 60
 Db 2 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 61
 Qy 61 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 119
 Db 62 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 120

Query Match 99.4%; Score 645; DB 3; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1,4e-64;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 60
 Db 2 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 61
 Qy 61 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 119
 Db 62 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 120

RESULT 3
 US-08-808-324-4
 Sequence 4, Application US/0880324
 Patent No. 624872
 GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil

APPLICANT: Thomas, Gerald R.
 APPLICANT: Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/808,324
 FILING DATE: Harewith
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617 876-5851
 TELEPHONE: 617 498-8260
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-808-324-4
 Query Match 99.4%; Score 645; DB 3; Length 120;
 Best Local Similarity 99.2%; Pred. No. 1,4e-64;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 60
 Db 2 PLATQCKEPEKSKALVNFKMGNDWIAFLTEFHCGLCEFLASLE 61
 Qy 61 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 119
 Db 62 PTHNAVITQANNSORSTPPACVTFPLSFSLTSDANNVVYKTEMVNSQCR 120

RESULT 4
 US-08-14030A-4
 Sequence 4, Application PC/TUS8414030A
 Patent No. 624872
 GENERAL INFORMATION: CS INSTITUTE, INC.
 APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PC/TUS84/14030A
 FILING DATE: Harewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

```

1 APPLICATION NUMBER: US 08/164,103
2 FILING DATE: 07-DEC-1993
3 APPLICATION NUMBER: US 08/717,780
4 INVENTOR: KATZ, MICHAEL
5 APPLICATION NUMBER: US 08/733,576
6 FILING DATE: 02-NOV-1994
7 ATTORNEY/AGENT INFORMATION:
8 NAME: KATZ, MICHAEL
9 TELEPHONE: 202/638-5000
10 REFERENCE/DOCKET NUMBER: 32,618
11 INFORMATION FOR SEQ ID NO: 1:
12 TYPE: amino acid
13 LENGTH: 120 amino acids
14 MOLECULE TYPE: protein
15 PCT/US94-140304-4
16
17 Query Match
18 Best Local Similarity 99.44; Score 645; DB 5; Length 120;
19 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
20
21 QY 1 PLATGQKRSKSLKARSKALVNFQMGKDWIPIEYAPRHSGLCEPFLSHLE 60
22 DB 2 PLATGQKRSKSLKARSKALVNFQMGKDWIPIEYAPRHSGLCEPFLSHLE 61
23 QY 61 PTHAVIOTLANSKDEPSTPCVPLRSPSLIFISANVVTGIDMAYVESCCR 119
24 DB 62 PTHAVIOTLANSKDEPSTPCVPLRSPSLIFISANVVTGIDMAYVESCCR 120
25
26 RESULT 5
27 Sequence 3, Application US/03289222E
28 Patent No. 610760
29 GENE/PROTEIN NAME:
30 APPLICANT: BOTTEN, GERTRUD
31 APPLICANT: BEINFELD, ROLF
32 TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TOP-B
33 TITLE OF INVENTION: FAMILY
34 CORRESPONDENCE ADDRESS:
35 ADDRESSEE: MIKALDO, MARCELSTEIN, MURRAY & ORAM LLP
36 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
37 CITY: WASHINGTON
38 STATE: DC
39 ZIP: 20005-5701
40 COMPUTER READABLE FORM:
41 MEDIUM TYPE: floppy disk
42 OPERATING SYSTEM: PC-DOS/MS-DOS
43 SOFTWARE: PatentIn Release #1.0, Version #1.25
44 CURRENT APPLICATION DATA: US 08/289,222E
45 FILING DATE: 25-AUG-1999
46 CLASSIFICATION: 424
47 PRIORITY INFORMATION:
48 APPLICATION NUMBER: US 08/289,222
49 FILING DATE: 12-AUG-1994
50 PRIOR APPLICATION DATA: US P 44 23 190,3
51 FILING DATE: 07-JUL-1994
52 PRIOR APPLICATION DATA:
53 APPLICATION NUMBER: SPO 92102324, 8
54 FILING DATE: 12-FEB-1993
55 NAME: KATZ, MICHAEL
56 FLOW APPLICATION DATA:

```

```

1 APPLICATION NUMBER: PCT/EP93/00350
2 FILING DATE: 12-FEB-1993
3 ATTORNEY/AGENT INFORMATION:
4 NAME: KATZ, MICHAEL
5 REGISTRATION NUMBER: 36,105
6 REFERENCE/DOCKET NUMBER: P564-9021
7 TELEPHONE: 202/638-5000
8 TELEFAX: 202/638-4810
9 INFORMATION FOR SEQ ID NO: 3:
10 TYPE: amino acid
11 LENGTH: 401 amino acids
12 MOLECULE TYPE: single
13 INFORMATION FOR SEQ ID NO: 4:
14 TYPE: amino acid
15 LENGTH: 401 amino acids
16 MOLECULE TYPE: protein
17 US-08-289-222E-3
18
19 Query Match
20 Best Local Similarity 99.44; Score 645; DB 3; Length 401;
21 Matches 118; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
22
23 QY 1 PLATGQKRSKSLKARSKALVNFQMGKDWIPIEYAPRHSGLCEPFLSHLE 40
24 DB 283 PLATGQKRSKSLKARSKALVNFQMGKDWIPIEYAPRHSGLCEPFLSHLE 342
25 QY 61 PTHAVIOTLANSKDEPSTPCVPLRSPSLIFISANVVTGIDMAYVESCCR 119
26 DB 343 PTHAVIOTLANSKDEPSTPCVPLRSPSLIFISANVVTGIDMAYVESCCR 401
27
28 RESULT 6
29 US-09-054-526E-3
30 Sequence 3, Application US/0905426E
31 Patent No. 6197550
32 GENE/PROTEIN NAME:
33 APPLICANT: HITTEN, GERTRUD
34 APPLICANT: BEINFELD, ROLF
35 APPLICANT: BEINFELD, ROLF
36 TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
37 TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
38 CORRESPONDENCE ADDRESS:
39 ADDRESSEE: MIKALDO, MARCELSTEIN, MURRAY & ORAM LLP
40 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
41 CITY: WASHINGTON
42 STATE: DC
43 ZIP: 20005-5701
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: floppy disk
46 OPERATING SYSTEM: PC-DOS/MS-DOS
47 SOFTWARE: PatentIn Release #1.0, Version #1.25
48 CURRENT APPLICATION DATA: US 09/054,526B
49 FILING DATE: 03-APR-1998
50 PRIOR APPLICATION DATA:
51 FILING DATE: US 08/289,222
52 FILING DATE: 12-AUG-1994
53 PRIOR APPLICATION DATA:
54 FILING DATE: US P 44 23 190,3
55 FILING DATE: 03-JUL-1994
56 PRIOR APPLICATION DATA:
57 APPLICATION NUMBER: SPO 92102324, 8
58 FILING DATE: 12-FEB-1993
59 PRIOR APPLICATION DATA:
60 APPLICATION NUMBER: PCT/EP93/00350
61 FILING DATE: 12-FEB-1993
62 NAME: KATZ, MICHAEL
63 FLOW APPLICATION DATA:

```

[illegible]

```

1 1 ZIP: 90067
2 1 COMPUTER READABLE FORM:
3 1 1. TITLE: PC-DOS/MS-DOS COMPATIBLE
4 1 2. APPLICANT: IBM PC compatible
5 1 3. ATTORNEY/AGENT INFORMATION:
6 1 4. FILING DATE: 31-MAY-1995
7 1 5. APPLICATION NUMBER: 08/093,144
8 1 6. REGISTRATION NUMBER: 31,678
9 1 7. CLASSIFICATION: 435
10 1 8. PUBLICATION NUMBER: 05/08/455,559
11 1 9. FILING DATE: 31-MAY-1995
12 1 10. APPLICATION NUMBER: 05/08/455,559
13 1 11. REGISTRATION NUMBER: 31,678
14 1 12. J.P. D., JOHN R.
15 1 13. NAME: WETHERELL, JR. PH.D., JOHN R.
16 1 14. ADDRESS: 4225 Executive Square, Suite 1400
17 1 15. CITY: La Jolla
18 1 16. STATE: CALIFORNIA
19 1 17. COUNTRY: USA
20 1 18. ZIP: 92037
21 1 19. COMPUTER READABLE FORM:
22 1 20. TITLE: IBM PC compatible
23 1 21. APPLICANT: IBM PC compatible
24 1 22. ATTORNEY/AGENT INFORMATION:
25 1 23. FILING DATE: 31-MAY-1995
26 1 24. APPLICATION NUMBER: 05/08/455,559
27 1 25. REGISTRATION NUMBER: 31,678
28 1 26. CLASSIFICATION: 435
29 1 27. PUBLICATION NUMBER: 05/08/455,559
30 1 28. FILING DATE: 31-MAY-1995
31 1 29. APPLICATION NUMBER: 05/08/455,559
32 1 30. REGISTRATION NUMBER: 31,678
33 1 31. J.P. D., JOHN R.
34 1 32. NAME: WETHERELL, JR. PH.D., JOHN R.
35 1 33. ADDRESS: 4225 Executive Square, Suite 1400
36 1 34. CITY: La Jolla
37 1 35. STATE: CALIFORNIA
38 1 36. COUNTRY: USA
39 1 37. ZIP: 92037
40 1 38. COMPUTER READABLE FORM:
41 1 39. TITLE: IBM PC compatible
42 1 40. APPLICANT: IBM PC compatible
43 1 41. ATTORNEY/AGENT INFORMATION:
44 1 42. FILING DATE: 31-MAY-1995
45 1 43. APPLICATION NUMBER: 05/08/455,559
46 1 44. REGISTRATION NUMBER: 31,678
47 1 45. CLASSIFICATION: 435
48 1 46. PUBLICATION NUMBER: 05/08/455,559
49 1 47. FILING DATE: 31-MAY-1995
50 1 48. APPLICATION NUMBER: 05/08/455,559
51 1 49. REGISTRATION NUMBER: 31,678
52 1 50. J.P. D., JOHN R.
53 1 51. NAME: WETHERELL, JR. PH.D., JOHN R.
54 1 52. ADDRESS: 4225 Executive Square, Suite 1400
55 1 53. CITY: La Jolla
56 1 54. STATE: CALIFORNIA
57 1 55. COUNTRY: USA
58 1 56. ZIP: 92037
59 1 57. COMPUTER READABLE FORM:
60 1 58. TITLE: IBM PC compatible
61 1 59. APPLICANT: IBM PC compatible
62 1 60. ATTORNEY/AGENT INFORMATION:
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; FEATURE:
; NAME/KEY: Protein
; SCORE: 98.64; Score 640; DB 5; Length 119;
; Mismatches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
PCT-US94-00657-13

Query Match
Sequence Similarity 98.64; Score 640; DB 5; Length 119;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 PLATROGKPSFKNKAERKALNFKMNDKMTIAPIETAPRCHLCEPLFASLE 60
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DB 61 PKNVAVTQTLNMSDPSPPFACVPELSPILSIDANNNVYKQEDNVESGCR 119
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DB 61 PKNVAVTQTLNMSDPSPPFACVPELSPILSIDANNNVYKQEDNVESGCR 119

RESULT 12
US-08-455-559-10
Sequence Similarity 98.64; Score 640; DB 1; Length 495;
Patent No. 5801014; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: BUNYU THANE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: COSTA MESA
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92627
COMPUTER: IBM compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/003,144
FILING DATE: 12-JAN-1993
AGENT/ATTORNEY INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
SOURCE CHARACTERISTICS:
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-559-10

Query Match
Sequence Similarity 98.64; Score 640; DB 1; Length 495;
Patent No. 5801014; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: BUNYU THANE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: COSTA MESA
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92627
COMPUTER: IBM compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/003,144
FILING DATE: 12-JAN-1993
AGENT/ATTORNEY INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
SOURCE CHARACTERISTICS:
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-559-10

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RESULT 13
US-09-145-060-10
Sequence Similarity 98.64; Score 640; DB 3; Length 495;
Patent No. 6245596; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: KUYU, THANE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 4225 Executive Square, Suite 1400
CITY: COSTA MESA
STATE: CA
COUNTRY: USA
ZIP: 92627
COMPUTER: IBM compatible
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: PARSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 12-JAN-1993
AGENT/ATTORNEY INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
SOURCE CHARACTERISTICS:
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-145-060-10

Query Match
Sequence Similarity 98.64; Score 640; DB 3; Length 495;
Patent No. 6245596; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: BUNYU THANE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: COSTA MESA
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92627
COMPUTER: IBM compatible
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: PARSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 12-JAN-1993
AGENT/ATTORNEY INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
SOURCE CHARACTERISTICS:
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-145-060-10

Query Match
Sequence Similarity 98.64; Score 640; DB 3; Length 495;
Patent No. 6245596; Pred. No. 2.9e-63;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: BUNYU THANE
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: COSTA MESA
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92627
COMPUTER: IBM compatible
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: PARSER for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 12-JAN-1993
AGENT/ATTORNEY INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
SOURCE CHARACTERISTICS:
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-145-060-10

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1 ZIP: 90667
 2 COMPUTER READABLE FORM:
 3 PATENT APPLICATION
 4 COMPUTER FILE NO. AVAILABLE
 5 OPERATING SYSTEM: PC-DOS/MS-DOS
 6 SOFTWARE: Patent Release #1.0, Version #1.25
 7 COMMUNICATIONS INFORMATION:
 8 FILING DATE: 1/12/94
 9 APPLICATION NUMBER: PCT/US94/00657
 10 CLASSIFICATION:
 11 NAME: MYERRELL, JR. PH.D., JOHN R.
 12 REGISTRATION NUMBER: 31,678
 13 REGISTRATION DATE: 1994-01-25
 14 TELECOMMUNICATIONS INFORMATION:
 15 TELEPHONE: 619/455-5100
 16 INFOTELEPHONE: 619/455-5110
 17 SEQUENCE CHARACTERISTICS: 10:
 18 LENGTH: 495 amino acids
 19 TOPOLOGY: single
 20 MOLECULE TYPE: protein
 21 PCT:US94-00657-10
 22
 23 Query Match: 98.6%; Score 640; DB 5; Length 495;
 24 Best Local Similarity 98.3%; Pred. No. 2.9e-63;
 25 Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 26
 27 QY 1 PAAQQRKYSNLAACSKALVFNKMGNDWIALEAFKCEFLFLEHLE 60
 28 DB 377 PAAQQRKYSNLAACSKALVFNKMGNDWIALEAFKCEFLFLEHLE 436
 29 QY 61 PTHNAVYQTLSNDSPTFPACVTFPLSPISLIFDGSANNVYKTEMVYSCGR 119
 30 DB 437 PTHNAVYQTLSNDSPTFPACVTFPLSPISLIFDGSANNVYKTEMVYSCGR 495

1 TELEPHONE: 714-760-0404
 2 TELEFAX: 714-760-9502
 3 INFORMATION FOR SEQ ID NO: 51:
 4 SEQUENCE CHARACTERISTICS:
 5 LENGTH: 102 amino acids
 6 STRANDNESS: single
 7 TOPOLOGY: linear
 8 MOLECULE TYPE: peptide
 9 ANTI-SENSE: NO
 10 FRAGMENT TYPE: C-terminal
 11 ORIGIN: SOURCE:
 12 US-08-335-383C-31
 13
 14 Query Match: 86.1%; Score 559; DB 1; Length 102;
 15 Best Local Similarity 86.4%; Pred. No. 1.9e-35;
 16 Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 17
 18 QY 18 CSRKALVFNKMGNDWIALEAFKCEFLFLEHLEPPTNAVYQTLSNDS 77
 19 DB 1 CSRKALVFNKMGNDWIALEAFKCEFLFLEHLEPPTNAVYQTLSNDS 60
 20 QY 78 STPTFAVTFEPTFLFDSANNVYKTEMVYSCGR 119
 21 DB 61 STPTFAVTFEPTFLFDSANNVYKTEMVYSCGR 102

Search completed: September 26, 2003, 18:00:22
 Job time : 30 secs

1 RESULTS 15
 2 US-08-335-383C-51
 3 Sequence 31, Application US/0833583C
 4 Patent No. 5653779
 5 GENETIC INFORMATION:
 6 APPLICANT: Moco Jr., Malcolm
 7 APPLICANT: Wang, Shouan
 8 APPLICANT: Kikba, Maile
 9 APPLICANT: Kikba, Maile
 10 TITLE OF INVENTION: ANTI-COSMALLING MORPHOGENETIC PROTEIN
 11 NUMBER OF SEQUENCES: 56
 12 CORRESPONDENCE ADDRESS:
 13 STREET: 620 Newport Center drive 16th Floor
 14 CITY: Newport Beach
 15 STATE: CA
 16 COUNTRY: USA
 17 ZIP: 92660
 18 COMPUTER READABLE FORM:
 19 NAME: Patent Release #1.0
 20 COMPUTER: IBM Compatible
 21 OPERATING SYSTEM: DOS
 22 SOFTWARE: Patented Version 1.5
 23 COMMUNICATIONS INFORMATION:
 24 APPLICATION NUMBER: US/08/335-383C
 25 FILING DATE:
 26 CLASSIFICATION: 435
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER:
 29 FILING DATE:
 30 NAME: MYERRELL, JR. PH.D., JOHN R.
 31 REGISTRATION NUMBER: 34,115
 32 REFERENCE/DOCCT NUMBER: NIH104.001A
 33 TELECOMMUNICATIONS INFORMATION:


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Query Match      98.5%; Score 640; DB 2; Length 495;
Best Local Similarity 98.3%; Pred. No. 1.5e-58;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 60
DB 377 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 436
QY 61 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 119
DB 437 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 495

RESULT 3
A:Species: Homo sapiens (man)
C:Dates: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000
C:Accession: F55452
E:Chang, S.C.; Boag, B.; Thomas, J.T.; Vukicovic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak, M. 269, 28227-28234, 1994
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily.
A:Accession: F55452; M01D:9450604; PMID:7961761
A:Status: Preliminary
A:Genetics: 1501 cDNA
A:Residues: 1-501 cDNA
A:Cross-references: Q8438940
A:Superfamily: inhibin

Query Match      98.5%; Score 639; DB 2; Length 501;
Best Local Similarity 98.3%; Pred. No. 1.9e-58;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 60
DB 383 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 442
QY 61 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 119
DB 443 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 501

RESULT 4
A:Species: Homo sapiens (human)
C:Dates: 10-Feb-1995 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C:Accession: F54296
E:Chang, S.C.; Boag, B.; Thomas, J.T.; Vukicovic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak, M. 269, 28227-28234, 1994
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily.
A:Accession: F54296; M01D:9450604; PMID:7961761
A:Status: Preliminary
A:Genetics: 1501 cDNA
A:Residues: 1-501 cDNA
A:Cross-references: Q8438940
A:Superfamily: inhibin

Query Match      98.5%; Score 639; DB 2; Length 501;
Best Local Similarity 98.3%; Pred. No. 1.9e-58;
Matches 117; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 60
DB 383 PLATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 442
QY 61 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 119
DB 443 PTHNVIOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 501

RESULT 5
A:Species: Homo sapiens (human)
C:Dates: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
C:Accession: F55452
E:Chang, S.C.; Boag, B.; Thomas, J.T.; Vukicovic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak, M. 269, 28227-28234, 1994
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily.
A:Accession: F55452; M01D:9450604; PMID:7961761
A:Status: Preliminary
A:Genetics: 1501 cDNA
A:Residues: 1-501 cDNA
A:Cross-references: Q8438940
A:Superfamily: inhibin

Query Match      81.4%; Score 528; DB 2; Length 436;
Best Local Similarity 76.9%; Pred. No. 5.4e-17;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 62
DB 320 ATGQKRSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPT 379
QY 63 NNAVITLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 119
DB 380 NNAVITLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 436

RESULT 6
A:Species: Homo sapiens (house mouse)
C:Dates: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C:Accession: S43296
E:Storm, R.E.; Ryba, N.J.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. 119
J. Biol. Chem. 269, 28227-28234, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the transforming growth factor-beta superfamily.
A:Accession: S43296; M01D:845850
A:Status: Preliminary
A:Genetics: 1501 cDNA
A:Residues: 1-151 cDNA
A:Cross-references: Q8438945; P01D:AA18770.1; P01D:848466
A:Superfamily: inhibin

Query Match      76.0%; Score 493; DB 2; Length 131;
Best Local Similarity 76.0%; Pred. No. 1.0e-10;
Matches 3; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY 7 GREGSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPTNAV 66
DB 39 GREGSKLNKSKALNFKVNGKMDWIAFLVFATFRCGICFFPLRSLEPTNAV 98
QY 61 IOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 119
DB 99 IOTLANSNDPSPTTACVPTPLSPISILFDANNNVTKQEDWYVSCGR 151

RESULT 7
A:Species: sea urchin (Strongylocentrotus purpuratus)
C:Dates: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999

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[illegible]

RESULT 11
 JH0689
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH0689
 R:Francis, P. H.; Richardson, M. K.; Shoa, A.; Nukachi, K.; Ueno, R.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early
 A:Reference number: JH0687; MDID:5237610; PMID:131675
 A:Accession: JH0688
 A:Molecule type: mRNA
 A:Residues: 1-401 <INS>
 A:Status: preliminary
 A:Superfamily: inhibin
 A:Experimental source: oocyte
 A:Cross-references: BML:G63426; NID:964887; PDB:CM45020.1; PDB:964588
 F:141,304,238,343,558/Binding site: carboxylate (asn) (covalent) status predicted
 Query Match 53.3%; Score 347; DB 2; Length 401;
 Best Local Similarity 52.1%; Pred. No. 3-8-28;
 Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;
 QY 4 TQGGSEKSLAR-----CSKALNFMKMGMDITAPETAFRHCZCFPLRSH 58
 DB 282 TRRSRSPQKQPEKMKHCRHSLSYDFSDVDMVIAVPTQATCCDCCFFLAHR 341
 QY 59 LPTNHAIVTQANSDPSTPPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 118
 DB 342 LNSTHAIIVTQANVNSV-SSIPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 400
 QY 119 R 119
 DB 401 R 401

RESULT 12
 bone morphogenetic protein 4 - African clawed frog
 N:Alternate names: BMP-4; ventralizing factor
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: JH3447
 R:Edble, L.; Howe, G.; Price, J. M.; Smith, J. C.
 Nature 375, 81-84, 1987
 A:Title: Bone morphogenetic protein 4: a ventralizing factor in early Xenopus developmen
 A:Reference number: JH3447; MDID:9348619; PMID:1442540
 A:Accession: JH3448
 A:Molecule type: nucleic acid
 A:Residues: 1-400 <MOD>
 A:Status: preliminary
 A:Superfamily: inhibin
 A:Experimental source: XTC cells
 A:Note: Sequence extracted from NCB backbone (NCBI:117127, NCBI:P:117128)
 Query Match 53.3%; Score 346; DB 2; Length 400;
 Best Local Similarity 52.1%; Pred. No. 3-8-28;
 Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;
 QY 4 TQGGSEKSLAR-----CSKALNFMKMGMDITAPETAFRHCZCFPLRSH 58
 DB 281 TRRSRSPQKQPEKMKHCRHSLSYDFSDVDMVIAVPTQATCCDCCFFLAHR 340
 QY 59 LPTNHAIVTQANSDPSTPPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 118
 DB 341 LNSTHAIIVTQANVNSV-ASIPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 399
 QY 119 R 119
 DB 400 R 400

RESULT 13
 bone morphogenetic protein 4 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: U00006
 R:Francis, P. H.; Richardson, M. K.; Brickell, P. M.; Tickle, C.
 Development 120, 209-218, 1994
 A:Title: A bone morphogenetic protein-4 cDNA encodes a signaling pathway that controls patterni
 A:Reference number: U00007; MDID:94163974; PMID:8119128
 A:Accession: U00008
 A:Status: preliminary
 A:Superfamily: inhibin
 A:Experimental source: gastrula (DB/DBE)/DB/DB
 A:Cross-references: BML:X75915; NID:947293; PDB:CM43514.1; PDB:947293
 F:120,342,377,529/Binding site: carboxylate (asn) (covalent) status predicted
 Query Match 53.3%; Score 346; DB 2; Length 405;
 Best Local Similarity 52.1%; Pred. No. 3-8-28;
 Matches 63; Conservative 21; Mismatches 31; Indels 6; Gaps 2;
 QY 4 TQGGSEKSLAR-----CSKALNFMKMGMDITAPETAFRHCZCFPLRSH 58
 DB 286 TRRSRSPQKQPEKMKHCRHSLSYDFSDVDMVIAVPTQATCCDCCFFLAHR 345
 QY 59 LPTNHAIVTQANSDPSTPPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 118
 DB 346 LNSTHAIIVTQANVNSV-SSIPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 404
 QY 119 R 119
 DB 405 R 405

RESULT 14
 decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
 C:Accession: J24158
 R:Padgett, R. W.; St. Johnston, R.D.; Gelbart, W.M.
 Nature 325, 81-84, 1987
 A:Title: The Drosophila pattern gene predicts a protein homologous to
 A:Reference number: J24158; MDID:8709408; PMID:3467201
 A:Accession: J24159
 A:Status: preliminary
 A:Superfamily: inhibin
 A:Cross-references: (B:M30116; NID:9157291; PDB:9157292
 C:Genetic PDB:9157292
 A:Experimental source: embryo
 A:Note: Sequence extracted from NCB backbone (NCBI:9157291, NCBI:P:9157291)
 F:120,342,377,529/Binding site: carboxylate (asn) (covalent) status predicted
 Query Match 53.0%; Score 344; DB 2; Length 588;
 Best Local Similarity 52.0%; Pred. No. 3-8-34;
 Matches 57; Conservative 24; Mismatches 21; Indels 2; Gaps 1;
 QY 5 TQGGSEKSLAR-----CSKALNFMKMGMDITAPETAFRHCZCFPLRSH 62
 DB 472 TRRSRSPQKQPEKMKHCRHSLSYDFSDVDMVIAVPTQATCCDCCFFLAHR 531
 QY 63 NHAIVTQANSDPSTPPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 119
 DB 532 NHAIVTQANSDPSTPPACYPFLPSLSTIPSDIANVYKOTEDVAVESCC 588
 RESULT 15
 JH0688

Search completed: September 26, 2003, 17:59:45
Job time : 40 secs